AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings of claims, in the application:

LISTING OF CLAIMS:

1-19. (Canceled)

20. (New) A method for the identification, isolation or separation of identical nucleic acid fragments from a mixture of at least two nucleic acid populations, comprising:

a) digesting separately nucleic acids of said at least two populations with at least one restriction enzyme;

b) ligating a blunt-ended adaptor sequence to the restriction fragments resulting from the digestion in step (a), said adaptor sequence having a unique 5' end sequence for each nucleic acid population;

c) mixing the ligation products resulting from the ligation in step (b), from said at least two nucleic acid populations each carrying adaptor sequences with unique 5' end sequences;

d) denaturing and re-hybridizing the mixture of nucleic acids resulting from the mixing in step (c) to generate a mixture comprising homoduplexes and heteroduplexes;

e) digesting perfectly matched blunt-ended homoduplexes by a blunt ended specific nuclease;

f) eliminating mismatched heteroduplexes with mismatch repair enzymes; and

g) identifying, isolating or separating fully-matched heteroduplexes, thereby identifying, isolating or separating nucleic acid fragments that are identical between said at least two nucleic acid populations.

21. (New) The method of claim 20, wherein the nucleic acid populations are human genomic DNA populations, from different subjects having a common trait of interest.

22. (New) The method of claim 20, wherein the nucleic acid populations comprise selected chromosome(s).

23. (New) The method of claim 20, wherein two or more nucleic acid populations from

different sources are used.

24. (New) The method of claim 20, wherein the adaptor sequence comprises a recognition site for mut HL.

25. (New) The method of claim 24, wherein the adaptor molecule is a 5-100 base long double-stranded DNA fragment comprising at least one GATC motif.

26. (New) The method of claim 20, wherein the adaptor sequence is labeled by a method selected from the group consisting of (i) adding a unique end sequence to each adaptor, (ii) adding a chemical activity to the adaptor which provides a means to distinguish between the ligation products from different nucleic acid populations and (iii) adding modified nucleotides into the adaptor allowing to distinguish between the ligation products from different nucleic acid populations.

27. (New) The method of claim 20, wherein the nuclease is exonuclease III.

28. (New) The method according to claim 20, wherein said adaptor sequences comprise unique 5' end sequences of at least 4 nucleotides up to 10 nucleotides.

29. (New) The method of claim 20, wherein, in step (f), mismatched nucleic acid fragments are eliminated by incubating the hybridization mixture with MutS, MutL and MutH.

30. (New) The method of claim 20, further comprising after step (e) a step of eliminating newly created single strands.

31. (New) The method of claim 30, wherein said step of eliminating newly created single strands comprises binding said strands to a single strand specific matrix.